

GenCore version 5.1.6  
Copyright (c) 1993 2003 CompuGen Ltd.

OM protein - protein search, using swi/model

Run on: June 25, 2003, 14:20:45 ; Search time 5.45349 Seconds  
(Without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613b-8

Perfect score: 582  
Sequence: 1 MDWMLTFQKKHLLNTRDVC.....TFCVTCENQAPVHEVGVC 105

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt.40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	538	92.4	104	1	RN30_RANPI
2	277	47.6	111	1	RNPO_RANCA
3	270.5	46.5	111	1	LECS_RANCA
4	254.5	43.7	111	1	RNPL_RANCA
5	139	23.9	119	1	RNP_IGUIG
6	121.5	20.9	145	1	ANGR_MOUSE
7	121.5	20.9	146	1	ANGI_CERAE
8	120	20.6	124	1	RNP_CALMU
9	117	20.1	148	1	ANGI_BOVIN
10	115	19.8	128	1	RNPB_CAVPO
11	114	19.6	128	1	RNP_MYOCO
12	113	19.4	124	1	RNP_BALAC
13	112.5	19.3	146	1	ANGI_MACMU
14	109.5	18.8	145	1	ANGI_MOUSE
15	109.5	18.8	146	1	ANGI_PAPHA
16	108	18.6	128	1	RNP_PROGU
17	107.5	18.5	155	1	ECBP4_MOUSE
18	107	18.4	125	1	ANGI_RABYT
19	107	18.4	128	1	RNP_HYDHY
20	107	18.4	146	1	ANGI_MITOA
21	105.5	18.1	147	1	RNLA_HUMAN
22	105	18.0	124	1	RNP_CHIBR
23	105	18.0	150	1	RNP_BOVIN
24	104	17.9	156	1	ECBP3_MOUSE
25	103	17.7	147	1	ANGI_HUMAN
26	103	17.7	147	1	ANGI_PANTR
27	102	17.5	124	1	RNP_AEPMF
28	102	17.5	124	1	RNP_ANTAM
29	102	17.5	124	1	RNP_HIPAM
30	102	17.5	124	1	RNP_SHEEP
31	101.5	17.4	123	1	ANGI_PIG
32	101.5	17.4	150	1	RNKG_SALSC
33	101	17.4	124	1	RNP_BOBBU

34	101	17.4	124	1	RNP_CONTA
35	101	17.4	124	1	RNP_GAZTH
36	100	17.2	123	1	ANG2_BOVIN
37	100	17.2	124	1	RNP_GIRCA
38	100	17.2	124	1	RNP_PIG
39	100	17.2	128	1	RNP_HYSCR
40	100	17.2	156	1	RNP_MYOGL
41	100	17.2	167	1	RNBR_BOVIN
42	99	17.0	124	1	RNP_CAMDR
43	99	17.0	128	1	RNP_HORSE
44	99	17.0	146	1	ANGI_SAGOE
45	98.5	16.9	155	1	ECPI_MOUSE

## ALIGNMENTS

RESULT 1	ID	RN30_RANPI	STANDARD:	PRT:	104 AA.
AC	P22069:				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-FEB-1995 (Rel. 31, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OC	Rana pipiens (Northern leopard frog).				
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:				
OC	Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae: Rana.				
OX	NCBI_TaxID=8404;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Embryo;				
RX	MEDLINE=91093131; PubMed=1985896;				
RA	Ardelt W., Mikulski S.M., Shogen K.:				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens				
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251(1991).				
RN	[2]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=93066156; PubMed=1438177;				
RA	Mosmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,				
RT	James M.N.G.:				
RT	"Comparative molecular modeling and crystallization of P-30 protein:				
RT	a novel antitumor protein of Rana pipiens oocytes and early				
RL	embryos.";				
RL	Proteins 14:392-400(1992).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RX	MEDLINE=94166079; PubMed=8120892;				
RA	Mosmann S.C., Ardelt W., James M.N.G.:				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an				
RT	amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY				
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR				
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH				
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PDB: 1ONC; 31-JAN-94.				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: PF00074; RNaseA; 1.				
DR	Prodom: PD000535; RNaseA; 1.				
DR	SMART: SM00092; RNase PC; 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.				
FT	MOD_RES	1			
FT	ACT_SITE	10			
FT	ACT_SITE	31			
FT	ACT_SITE	97			
FT	DISULFID	19			
FT	DISULFID	30			
FT	DISULFID	48			

```

FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA: 11845 MW: 22A753C2F9E566B4 CRC64;

Query Match 92.4%; Score 538; DB 1; Length 104;
Best Local Similarity 93.3%; Pred. No. 1e-51;
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKNVLT 61
DB 1 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKNVLT 60
OY 62 FEFYLSDCNVTSPCKYKRLKSTIFCYTCENQAPVHVGHC 105
DB 61 SFEYLSDCNVTSPCKYKRLKSTINFCVTCENQAPVHVGVC 104

RESULT 2
RNPO_RANCA STANDARD: PRT: 111 AA.
ID RNPO_RANCA
AC P11916:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding
leucin) (SBL-C).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN 111
RP TISSUE=Egg;
RC MEDLINE=87299649; PubMed=3304421;
RA Tiltani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs."
RL Biochemistry 26:2189-2194(1987).
RN
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RL catesbeiana (bullfrog) oocytes."
RL Nucleic Acids Res. 20:1371-1377(1992).
RN
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Tiltani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RL catesbeiana eggs."
RL Glycobiology 3:37-45(1993).
RN
RP STRUCTURE BY NMR.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

```

```

RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
CC RESIDUES WITH A 3' FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
CC AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTIN IN FROG EGGS
CC MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG
CC EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING
CC NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND
CC HUMAN ORIGIN.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A27121; A27121.
DR PDB: 1BC4; 28-OCT-98.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR ProDom: PD000535; RNaseA.
DR SMART: SM00092; RNase_Pc.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
SQ SEQUENCE 111 AA: 12464 MW: 0BC9E5F5729ECF4 CRC64;

Query Match 47.6%; Score 277; DB 1; Length 111;
Best Local Similarity 47.7%; Pred. No. 2.3e-23;
Matches 53; Conservative 16; Mismatches 34; Indels 8; Gaps 3;

OY 2 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKN 57
DB 1 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKN 59
OY 58 VTFEFYLSDCNVTSPCKYKRLKSTIFCYTCENQAPVHVGHC 105
DB 60 VLSITRFQNLCTKRISITPRCPYSSKRTETNYICVKNQAPVHVGIGRC 110

RESULT 3
LECS_RANJA STANDARD: PRT: 111 AA.
ID LECS_RANJA
AC P18839:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese redbellied frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN 111
RP TISSUE=Egg;
RC MEDLINE=91035319; PubMed=2229005;
RA Kamliya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Tiltani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: JX0120; JX0120.

```

DR HSSP: P11916; 1BC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA. 1.  
 DR ProDom: PD000535; RNaseA. 1.  
 DR SMART: SM00092; RNase\_Pc. 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC. 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; lectin.  
 FT MOD\_RES 1 1  
 FT ACT\_SITE 10 10 PYROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 35 35 BY SIMILARITY.  
 FT ACT\_SITE 103 103 BY SIMILARITY.  
 FT ACT\_SITE 19 72 BY SIMILARITY.  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97  
 FT DISULFID 94 111  
 SO SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 46.58; Score 270.5; DB 1; Length 111;  
 Best Local Similarity 43.28; Pred. No. 1,2e-22;  
 Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

QY 2 QDMVTFQKHLTNRDVCNNILSTNLF---HCKDKNTFYSPREPVAICGKIASKN 57  
 1 QNNAKFOEKHIDPNTSNCNTIMDKSIYVGCKERNFTLISATTVKAICSGASTNRN 60  
 DB 58 VLTTFEFLSDC---NVTSPCKKYLKSTTFECVTCENQAPVHFVGVGHC 105  
 61 VLTTRQLNTCIRSATAPRCPYNSRTETNVICVCKENLPIVHFAIGRC 111

RESULT 4  
 RNP\_LANCA  
 ID RNP\_LANCA STANDARD; PRT: 111 AA.  
 AC P14626;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.  
 NC NCB1\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=90130374; Pubmed=2613682;  
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver."  
 RL J. Biochem. 106:729-735(1989).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSSP: P11516; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA. 1.  
 DR ProDom: PD000535; RNaseA. 1.  
 DR SMART: SM00092; RNase\_Pc. 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC. 1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT MOD\_RES 1 1  
 FT ACT\_SITE 10 10 PYROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 35 35 BY SIMILARITY.  
 FT ACT\_SITE 104 104 BY SIMILARITY.  
 FT DISULFID 19 72 BY SIMILARITY.  
 FT DISULFID 34 82 BY SIMILARITY.  
 FT DISULFID 52 97 BY SIMILARITY.  
 FT DISULFID 94 111 PROBABLE.  
 SO SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 43.7%; Score 254.5; DB 1; Length 111;  
 Best Local Similarity 41.44; Pred. No. 6,3e-21;  
 Matches 46; Conservative 19; Mismatches 39; Indels 7; Gaps 2;

QY 2 QDMVTFQKHLTNRDVCNNILSTNLF---HCKDKNTFYSPREPVAICGKIASKN 57  
 1 QNNAKFOEKHIDPNTSNCNTIMDKSIYVGCKERNFTLISATTVKAICSGASTNRN 60  
 DB 58 VLTTFEFLSDC---NVTSPCKKYLKSTTFECVTCENQAPVHFVGVGHC 105  
 61 ELSTTSFKLNTCIRDSITPRCPYHPSDDNNKICVCKEQLPIVHFAIGRC 111

RESULT 5  
 RNP\_IGUG  
 ID RNP\_IGUG STANDARD; PRT: 119 AA.  
 AC P80287;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).  
 OS Iguana iguana (Common Iguana).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosaurs; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
 NC NCB1\_TaxID=8517;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=94139745; Pubmed=8307028;  
 RA Zhao W., Beintema J.J., Hofsteenge J.;  
 RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic ribonuclease."  
 RL Eur. J. Biochem. 219:641-646(1994).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSSP: P00656; 1L50.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA. 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA. 1.  
 DR SMART: SM00092; RNase\_Pc. 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC. 1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT MOD\_RES 1 1  
 FT DISULFID 25 80 PYROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 39 91 BY SIMILARITY.  
 FT DISULFID 57 106 BY SIMILARITY.  
 FT ACT\_SITE 10 10 BY SIMILARITY.  
 FT ACT\_SITE 40 40 BY SIMILARITY.  
 FT ACT\_SITE 113 113 BY SIMILARITY.  
 SO SEQUENCE 119 AA; 13324 MW; 6072PFB5B7B15BD5A CRC64;

Query Match 23.9%; Score 139; DB 1; Length 119;  
 Best Local Similarity 29.8%; Pred. No. 2,3e-08;  
 Matches 34; Conservative 19; Mismatches 45; Indels 16; Gaps 5;

QY 2 QDMVTFQKHLTNRDVCNNILSTNLF---HCKDKNTFYSPREPVAIC--K 50  
 1 QNNAKFOEKHIDPNTSNCNTIMDKSIYVGCKERNFTLISATTVKAICSGASTNRN 60  
 DB 51 GIASKNVLTTFEFLSDC---NVTSPCKKYLKSTTFECVTCENQAPVH 99  
 61 GTHVEDMLYDSNESFDLTDCKNVCGTAPSSCKYNGTGTRIRIRIACGNNQPVH 114

RESULT 6  
 ANGR\_MOUSE  
 ID ANGR\_MOUSE STANDARD; PRT: 145 AA.

AC 064438;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Angiogenin-related protein precursor.  
GN ANGRP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129; TISSUE=Liver;  
RX MEDLINE=96079109; PubMed=8530072;  
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;  
RT "The mouse angiogenin gene family: structures of an angiogenin-related  
protein gene and two pseudogenes.";  
RL Genomics 29:200-206(1995).  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U22519; AAA91367.1; -  
DR HSSP: P03950; 1A4Y.  
DR MCD: MGI104984; Angrp.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA.1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR ProDom: PD000535; RNaseA.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR PROSITE: PS00127; RNase\_PANCREATIC.1.  
KW Signal; Hydrolase; Nuclease; Endonuclease.  
FT SIGNAL 1 24  
FT CHAIN 25 145 ANGIOGENIN-RELATED PROTEIN.  
FT MOD\_RES 25 25 PYROGLUTAMINE CARBOXYLIC ACID (BY  
FT ACT\_SITE 37 37 BY SIMILARITY).  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 137 137 BY SIMILARITY.  
FT DISULFID 50 104 BY SIMILARITY.  
FT DISULFID 63 115 BY SIMILARITY.  
FT DISULFID 81 130 BY SIMILARITY.  
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429CAD CRC64;  
Query Match 20.9%; Score 121.5; DB 1; Length 145;  
Best Local Similarity 36.8%; Pred. No. 2.3e-06;  
Matches 28; Conservative 11; Mismatches 30; Indels 7; Gaps 3;  
QY 31 CKDKNTFTYRPREYKAIC--KGIASKNV-LTFEYFLSDCNVTSR---PCKYKILKS 83  
DB 63 CKDVNTFTIHDTKNKIKICKGSPYGRNLRISKSPQVYTTCHKGRSPRCRYRASKG 122  
OY 84 TTFEYVTCENQAPYHF 99  
DB 123 FRYIIICENGMPVHF 138  
RESULT 7  
ANGI\_CERAE STANDARD; PRT: 146 AA.  
AC Q8WNG6;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).  
GN ANG OR RNASE5.  
OS Cercopithecus aethiops (Green monkey) (Givet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecinae; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in  
RT primate evolution.";  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND  
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AF441664; AL61646.1; -  
DR KW Hydrolase; Nuclease; Angiogenesis;  
KW Protein synthesis inhibitor; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 146 ANGIOGENIN.  
FT MOD\_RES 25 25 PYROGLUTAMINE CARBOXYLIC ACID (BY  
FT ACT\_SITE 37 37 BY SIMILARITY).  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 138 138 BY SIMILARITY.  
FT DISULFID 50 105 BY SIMILARITY.  
FT DISULFID 63 116 BY SIMILARITY.  
FT DISULFID 81 131 BY SIMILARITY.  
SQ SEQUENCE 146 AA; 16444 MW; 27860112E85B8DF9 CRC64;  
Query Match 20.9%; Score 121.5; DB 1; Length 146;  
Best Local Similarity 29.7%; Pred. No. 2.3e-06;  
Matches 30; Conservative 17; Mismatches 31; Indels 23; Gaps 4;  
QY 6 TPOKKHLTNRDVCNNILSTNLFHCKDKNTFTYRPREYKAIC--KGIASKNV-LTT 61  
DB 53 TMRRHITSP-----CKDINTFTIHGRHIIKAIKAGDENGPNYGRNLRISK 97  
OY 62 FEFLYSDCNVTS---RPCKYKILKSYTTCVVCENAPYH 98  
DB 98 SPFOVYTCNLGSGSPRCYRATGRSRNITVGCENGLPVH 138  
RESULT 8  
RNP\_GALMU STANDARD; PRT: 124 AA.  
AC P00680;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
GN RNASE1 OR RNS1.  
OS Galea musteloides (Cuis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Galea.  
OX NCBI\_TaxID=10146;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=87036770; PubMed=6571219;

```

RA MEDLINE=89375344; PubMed=2775757;
RT Bond M.D., Striydom D.J.;
RT "Amino acid sequence of bovine angiogenin.";
RL Biochemistry 28:6110-6113(1989).
RN [4]
RP CHARACTERIZATION, AND SEQUENCE OF 25-55.
RC TISSUE-plasma:
RX MEDLINE=89118214; PubMed=3064806;
RA Bond M.D., Vallee B.L.;
RT "Isolation of bovine angiogenin using a placental ribonuclease
RT inhibitor binding assay.";
RL Biochemistry 27:6282-6287(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=95224057; PubMed=7708754;
RA Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
RT "Crystal structure of bovine angiogenin at 1.5-A resolution."
RL Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE=96280645; PubMed=8688423;
RA Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT resonance spectroscopy.";
RL Biochemistry 35:8870-8880(1996).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS. BINDS TIGHTLY TO PLACENTAL
CC RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: SERUM, AND MILK
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL: AF135124; AAC47631.1;
CC PIR: A32474; A32474.
CC PDB: 1AGT; 03-APR-96.
CC PDB: 1GTO; 07-DEC-96.
CC DR InterPro: IPR001427; RNaseA.
CC DR Pfam: PF00074; RNaseA; 1.
CC DR PRINTS: PR00794; RIBONUCLEASE.
CC DR PRODOM: PD000535; RNaseA; 1.
CC DR SMART: SM00092; RNase.Pc; 1.
CC DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
CC KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
CC Protein synthesis inhibitor; Signal; 3D-structure.
CC FT SIGNAL 1 23
CC FT CHAIN 24 148 ANGIOGENIN-1.
CC FT ACT_SITE 37 37
CC FT ACT_SITE 64 64
CC FT ACT_SITE 138 138
CC FT DISULFID 50 105
CC FT DISULFID 63 116
CC FT DISULFID 81 131
CC SQ SEQUENCE 148 AA; 16969 MW; B7999124CBB523DD CRC64;
CC -----
Query Match 20.1% Score 117; DB 1; Length 148;
Best Local Similarity 32.7%; Pred. No. 7.2e-06;
Matches 32; Conservative 14; Mismatches 32; Indels 20; Gaps 5;

```

Db 47 DEXCFNMKNRRLTRPCCKDNTEFHGNKNDKADICEDRNGOPYRGDLRISKS-----EFQ 101  
 QY 66 LSDC---NWTSR-PCKYKLLKSTITFCVNCENAPVHF 99  
 Db 102 ITICKKHGSSRPPCRYGATEDSRVYVGCENGLPVHF 139

RESULT 10  
 RNP\_CAVPO STANDARD: PRT: 128 AA.  
 ID RNP\_CAVPO  
 AC P00679:  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB)  
 OS Cavia porcellus (Guinea pig)  
 OS Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavilidae; Cavia.  
 OC NCBI\_TaxID=10141;  
 RN (1)  
 RP SEQUENCE:  
 RC TISSUE-Pancreas;  
 RX MEDLINE=77185023; PubMed=862624;  
 RA van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,  
 Beintema J.J.;  
 RT "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary  
 structure and glycosylation."  
 RL Eur. J. Biochem. 75:91-100(1977).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: A00826; NRCPB.  
 DR HSSP: P00656; ISRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR SMART: PS00127; RNase\_PANCREATIC; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 65 72 BY SIMILARITY.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).  
 FT VARIANT 64 64 L -> P.  
 SQ SEQUENCE 128 AA; 14406 MW; A2F4101A1A33E93B CRC64;

Query Match 19.8%; Score 115; DB 1; Length 128;  
 Best Local Similarity 25.9%; Pred. NO. 1e-05;  
 Matches 30; Conservative 25; Mismatches 39; Indels 22; Gaps 7;

QY 5 LTFQKHL-----TTRVDCCNHL---STNLFHCKDKNTFLYSRPEVKAIC--KGIT 53  
 Db 6 MFQROHMDPEGSPSSNSN-CVMMIRRMTOGRCKPVNTEVHEPLADYQAVCFQKNVL 64  
 QY 54 ASKNVLTTFEYF---LSDCNVTSRP---CKYKLLKSTITFCVNCENQ--APVHF 99  
 Db 65 CKNGQTCNQCYSRMTITDCRVTSSSKFPCSRMSQAKSITVACEGDPYVPHF 120

RESULT 11  
 RNP\_MYOCO STANDARD: PRT: 128 AA.  
 ID RNP\_MYOCO  
 AC P00676;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).  
 GN RNASEL OR RNSL  
 OS Myocastor coypus (Coypu) (Nutria).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Myocastoridae;  
 OC Myocastor.  
 OC NCBI\_TaxID=10157;  
 RN (1)  
 RP SEQUENCE:  
 RC TISSUE-Pancreas;  
 RX MEDLINE=77065676; PubMed=999896;  
 RA van den Berg A., van den Hende-Timmer L., Beintema J.J.;  
 RT "Isolation, properties and primary structure of coypu and chinchilla  
 pancreatic ribonuclease."  
 RL Biochim. Biophys. Acta 453:400-409(1976).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-  
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P  
 with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR PIR: A00822; NRCU.  
 DR HSSP: P00656; ISRN.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA; 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA; 1.  
 DR SMART: SM00092; RNase\_Pc; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
 FT DISULFID 26 84 BY SIMILARITY.  
 FT DISULFID 40 95 BY SIMILARITY.  
 FT DISULFID 58 110 BY SIMILARITY.  
 FT DISULFID 65 72 BY SIMILARITY.  
 FT ACT\_SITE 12 12 BY SIMILARITY.  
 FT ACT\_SITE 41 41 BY SIMILARITY.  
 FT ACT\_SITE 119 119 BY SIMILARITY.  
 FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .).  
 SQ SEQUENCE 128 AA; 14267 MW; 4E924E52B445832 CRC64;

Query Match 19.6%; Score 114; DB 1; Length 128;  
 Best Local Similarity 28.2%; Pred. NO. 1.3e-05;  
 Matches 33; Conservative 19; Mismatches 37; Indels 28; Gaps 7;

QY 7 FQKHL-----TTRVDCCNHL---STNLF--HCKDKNTFLYSRPEVKAICGIASKNV 58  
 Db 8 FERQHDHSRSPSTNPNYCNEMKSRMTQGRCKPVNTEVHEPLADYQAVC---FQKNV 63  
 QY 59 L-----TTFEYLSDCNVTSRP---CKYKLLKSTITFCVNCENQ--APVHF 99  
 Db 64 LCKNGQTCNQCYSNMHITDCRVTSSSDYPNCSYRTSQRKSLVAVCEGDPYVPHF 120

RESULT 12  
 RNP\_BALAC STANDARD: PRT: 124 AA.  
 ID RNP\_BALAC  
 AC P00673;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).  
 GN RNASEL OR RNSL  
 OS Balaeoptera acutorostrata (Mink whale) (Lesser rorqual).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;  
 OC Balaeopteridae; Balaeoptera.  
 OC NCBI\_TaxID=9767;  
 RN (1)  
 RP SEQUENCE:  
 RC TISSUE-Pancreas;  
 RX MEDLINE=76277855; PubMed=962870;  
 RA Emmens M., Welling G.W., Beintema J.J.;

"The amino acid sequence of pike-whale (lesser-tongual) pancreatic ribonuclease.";  
RL Biochem. J. 157:317-323(1976).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: PANCREAS.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR PIR: A00818; NEMHK.  
DR HSSP: P00656; 1SRN.  
DR InterPro: IPR01427; RNaseA.  
DR Pfam: PF00074; RNaseA.1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR ProDom: PD000535; RNaseA.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC.1.  
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
FT DISULFID 26 84 BY SIMILARITY.  
FT DISULFID 40 95 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 65 72 BY SIMILARITY.  
FT ACT\_SITE 12 12 BY SIMILARITY.  
FT ACT\_SITE 41 41 BY SIMILARITY.  
FT ACT\_SITE 119 119 BY SIMILARITY.  
FT CARBOHYD 76 76 N-LINKED (GLCNAC, .) IN 30% OF THE MOLECULES.  
SO SEQUENCE 126 AA; 14125 MW; F57475459F697E20 CRC64;  
Query Match 19.4%; Score 113; DB 1; Length 124;  
Best Local Similarity 26.9%; Pred. No. 1.6e-05;  
Matches 32; Conservative 16; Mismatches 43; Indels 28; Gaps 6;  
QY 5 LTFQKHLTRFDYD-----CNHILSTNLF--HCKDKNFTYSRPEPKAICKGIATSK 56  
DB 6 MKFOHMDGSGSPNNPNYCNQMMRRKKTGRCRPFVTFVHESLEDAVAC---SQR 61  
57 NVL-----TTFEYLSDCNVTSP--CKYKLRKSTTFCTVCENQ--APVHF 99  
62 NVLCNKGRTNCEYNSNTMHTDCRQCGSSKYPKCAVTKSKKHHIYACGNGYVPHF 120  
RESULT 13  
ANGI\_MACMU STANDARD: PRT; 146 AA.  
AC O8RN63;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiogenin precursor (EC:3.1.27.-) (Ribonuclease 5) (Rnase 5).  
GN ANG OR RNASE5.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
OX NCBI\_Taxid=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in primate evolution."  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR EMBL: AF41667; AAL61649.1;  
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
KW Protein synthesis inhibitor; Signal.  
FT SIGNAL 1 24 BY SIMILARITY.  
FT CHAIN 25 146 ANGIOGENIN.  
FT MOD\_RSS 25 25 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).  
FT ACT\_SITE 37 37 BY SIMILARITY.  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 138 138 BY SIMILARITY.  
FT DISULFID 50 105 BY SIMILARITY.  
FT DISULFID 63 116 BY SIMILARITY.  
FT DISULFID 81 131 BY SIMILARITY.  
SO SEQUENCE 146 AA; 16301 MW; E39A89215DB2A244 CRC64;  
Query Match 19.3%; Score 112.5; DB 1; Length 146;  
Best Local Similarity 27.7%; Pred. No. 2.2e-05;  
Matches 28; Conservative 17; Mismatches 33; Indels 23; Gaps 4;  
QY 6 TPOKHLTRFDYDNNILSTNLFHCKDKNFTYSRPEPKAIC--GGIASKNV-LTP 61  
DB 53 TMRRHILTSF-----CKDINTFVGNHNRHITAIICDGENSPYCGNLRIST 97  
QY 62 FEFYLSDCNVTSP--RPCKYKLRKSTTFCTVCENQAPVH 98  
DB 98 SPFOYTTCKLRGSGPPRCQYRATRGSRNIVGCGENLPVH 138  
RESULT 14  
ANGI\_MOUSE STANDARD: PRT; 145 AA.  
AC P21570;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiogenin precursor (EC:3.1.27.-).  
GN ANG.  
OS Mus musculus (mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91025023; PubMed=2222458;  
RA Bond M.D., Vallee B.L.;  
RT "Isolation and sequencing of mouse angiogenin DNA."  
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).  
RN [2]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Serum;  
RX MEDLINE=93192291; PubMed=8448182;  
RA Bond M.D., Strydom D.J., Vallee B.L.;  
RT "Characterization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and regions."  
RL Biochem. Biophys. Acta 1162:177-186(1993).  
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

